

Figure 1

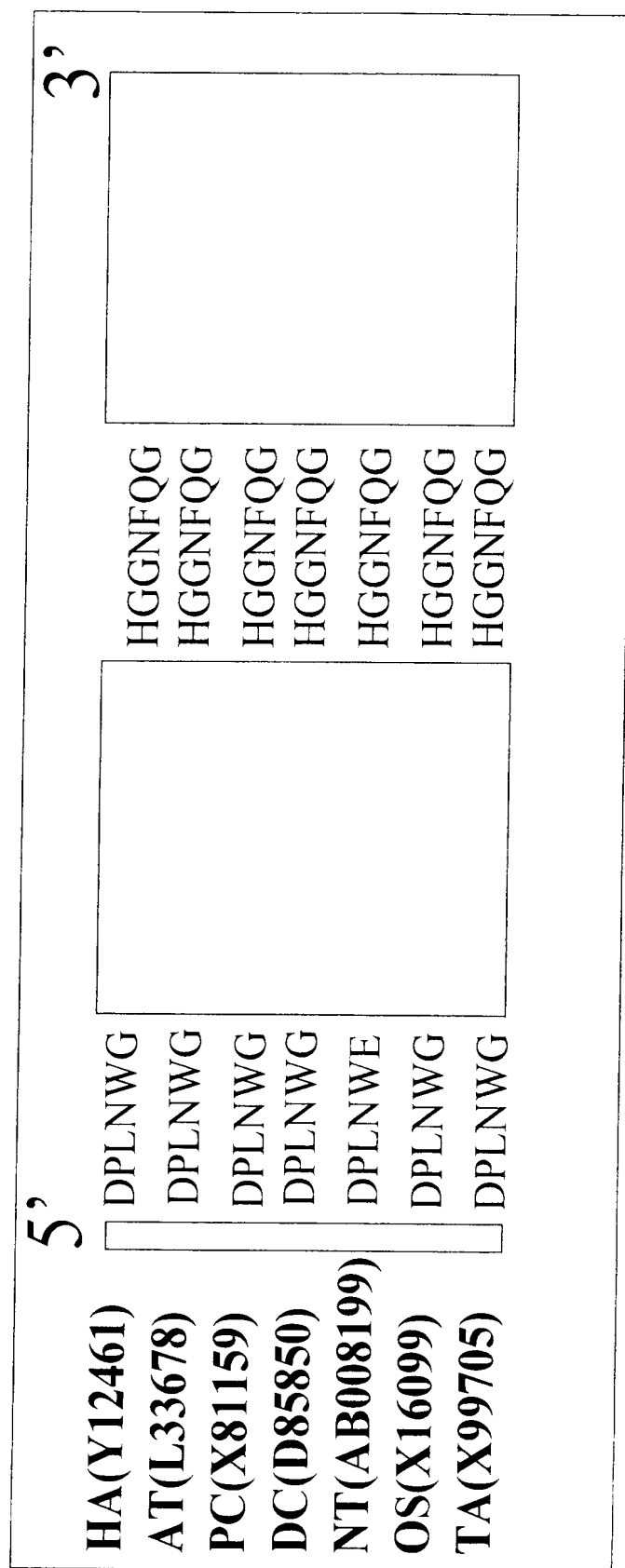


Figure 2

RT-PCR products

0	2 hrs		20 hrs		LsPAL2
c	c	w	c	w	

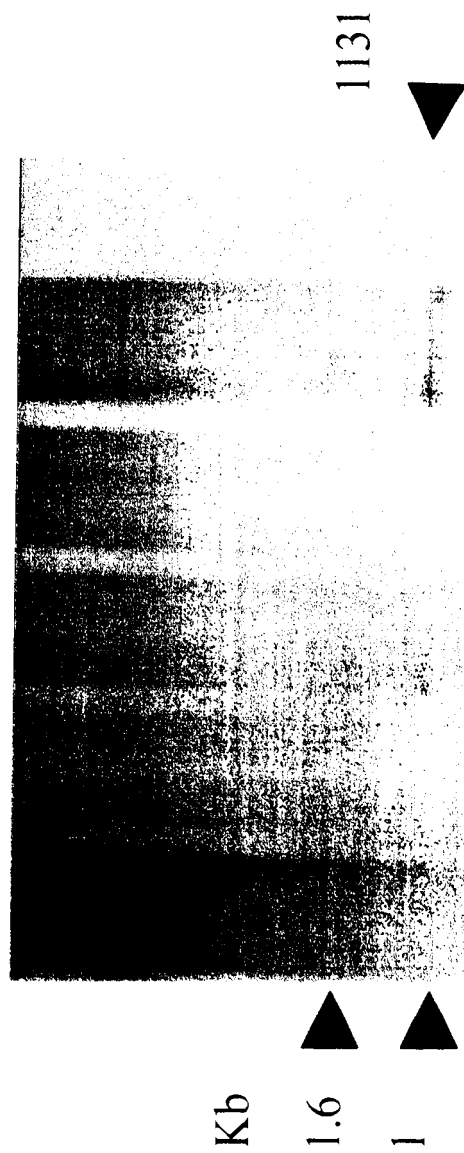


Figure 3

Domains

DPLNW

HGGNFQG

RT-PCR

3' RACE

5' RACE

Figure 4

PAL1

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1 GAGCAATCTG ATCAATACCC ATTCACGCAC AAAGAGTGTG AGTCTAGTGT GTGAAGAAGT
61 ACACAATTAG ATTGTTCTTG TTTCTTTGAT CTATAGTCTA CAATCTGTAT AAATAATAAT
121 GGAGAACGGT AATCACGTTA ATGGAGTCGT TAATGAGTTG TGCATCAAGG ATCCATTGAA
181 CTGGGGAGTT GCAGCGGAGG CGTTGACCGG AAGTCACCTT GATGAGGTGA AGAAGATGGT
241 TGC GGAGTTC AGAAAGCCGG TGGTGAAGCT CGGAGGAGAG ACGCTTACAG TTTCTCAGGT
301 GCGGGGGATC GCAGCTGCTA ATGACAGTGA CACCGTGAAG GTGGAGCTGT CGGAAGCCGC
361 GAGGGCTGGA GTTAAGGCGA GTAGTGATTG GGTATGGAG AGCATGAATA AAGGAACTGA
421 TAGTTATGGT GTCACCACCG GCTTCGGCGC CACCTCTCAC CGGAGAACTA AGCAAGGCCG
481 TGCTTTACAG AAGGAGCTCA TTAGATTTTT GAACGCCGGA ATATTCGGCA ATGGAACGGA
541 AACAGCCAC ACACTTCAC ATTCAGCCAC CAGAGCCGCC ATGATCGTCA GAATCAACAC
601 CCTCCTCAG GGTACTCCG GCATCCGATT CGAGATCTTG GAAGCCATCA CCAAGTTCCT
661 TAACAACAAC ATCACCCCTT GTTTACCCCT CCGTGGAACC ATCACCGCCT CCGGTGACCT
721 TGTCCCATTA TCATACATCG CCGGCCTCTT AACC GGCCGC CCAACTCCA AAGCCGTTGG
781 CCCCACCGGA GAAGTCCTCA ATGCCGAAAA GGCCTTCGCT GCAGCCGGAG TTGAAGGTGG
841 GTTCTTCGAG TTACAGCCGA AAGAAGGGCT AGCACTTGT AACGGCACCG CCGTGGGGTC
901 CGGGATGGCT TCCATGGTTC TATTTGATGC TAATGTA CTGCGTTGTTGT CGGAAGTGT
961 ATCGGCGATC TTCGCTGAGG TTATGCAAGG GAAGCCGGAG TTTACCGATC ACTTGACACA
1021 CAAATTGAAG CATCACCCCTG GTCAAATCGA GCGGCGGGCG ATCATGGAGT ATATTTTGA
1081 CGGAAGCGAT TACGTCAAGG CGGCGCAAAA GGTCCACGAA ATGGACCCGT TACAGAAAAC
1141 AAAACAAGAT CGTTATGCTC TCCGTACATC TCCCAATGG CTCGGACCTC AAATCGAAGT
1201 AATCCGATCA TCAACCAAAA TGATCGAGAG GGAAATCAAT TCCGTCAACG ACAACCCATT
1261 GATCGACGTT TCCAGAAACA AAGCTTTACA CCGTGGAAC TTCCAAGGAA CCCCATCGG
1321 AGTTTCCATG GACAACACCC GTCTCGCCAT TGCTGCAATC GGAAAACTCA TGTTGCTCA
1381 ATTTTCTGAG CTGGTTAACG ATTTCTACAA CAATGGATTA CCATCGAATC TCTCCGGTGG
1441 ACGTAACCCT AGTTTGGACT ACGGGTTCAA AGGTGGAGAA ATCGCCATGG CTTCTTACTG
1501 TTCTGAGCTT CAGTTTCTCG CAAATCCAGT CACCAACCAT GTTCAAAGCG CCGAACAACA
1561 CAATCAAGAC GTTAATTCTC TCGGATTAAT TTCAGCGAGG AAAACCGCAG AAGCAGTCCA
1621 CATCTTAAAA CTCATGTCGT CGACATACTT AGTCGCTCTA TGCCAATCCA TCGATTTACG
1681 CCATTTGGAA GAGAACATGA AATCGACAGT GAAGAACACC GTAAGCCAAG TCGCGAAAAA
1741 GGTCCTCACC ATGGGCGTCA ACGGCGAGCT CCACCCGTCG AGATTCTGCG AGAAAGATCT
1801 CCTCCGTGTT GTTGATCGTG AATACGTCTT CGCTTACATC GACGACGTTT GCAGCGGCAC
1861 ATACCCATTA ATGCAGAAGC TCCGACAGGT TCTGGTCGAC CACGCTCTAA ACAACGGCGA
1921 AACGGAGAAG AACACTAACA CCTCCATCTT CCAAAAGATC GCTACCTTCG AAGAAGAATT
1981 GAAAGTCCTG TTACCGAAAAG AAGTTGAAGG TGTTAGAATC GCTTATGAGA ATGATACATT
2041 GTCGATTCCA AACAGGATTA AAGCTTGCAG ATCGTACCCG TTGTATAGGT TTGTAAGGGA
2101 GGAGCTCGGC AGAGGGTTTT TGACCGGAGA AAAGGTGACG TCGCCGGGAG AGGAGTTCGA
2161 CAGGGTGTTT ACGGCGATGT GCAAAGGTCA AATTATTGAT CCGTTGTTGG AGTGTCTTGG
2221 AGGGTGGAAT GGGGAACCTC TTCCAATATG TTAGGAAAGT GAGTGTGAAA CCGTTTGAAT
2281 TGTATTTGTA ATATTCTGTT TTTTTTTTTT TTTTAAAT TTTATTGCA TTTAATATCT
2341 CATCAAAGAC TTCCACTTTC AAGTGTGGTG TATGTGGTTG TAAATCATAT ATATTAACCT
2401 ATTATTTTGT CTAACAAAAA AAAAAAAAAA AAAAAAAAAA AA

```

Figure 5

Sequence I.D. No. 3

PAL1

translation="MENG NHVNGV VNELCIKDPLNWGVAAEALTGSHLDEVKKMVAEFRKPVV
KLGGETLTVSQVAGIAAANDSDTVKVELSEARAGVKASSDWVMESMNKGTDSYGVT
TGFGATSHRRTKQGGALQKELIRFLNAGIFGNGTETSHTLPHSATRAAMIVRINTLLQGY
SGIRFEILEAITKFLNNNITPCLPLRGTTASGDLVPLSYIAGLLTGRPN SKAVGPTGEVLN
AEKAFAAAGVEGGFFELQPKEGLALVNGTAVGSGMASMVLFDANVLALLSEVLSAIFA
EVMQ GKPEFTDHLTHKLKHHPGQIEAAIMEYILDGSDYV KAAQKVHEMDPLQKPKQD
RYALRTSPQWLGPQIEVIR SSTKMIEREINSVNDNPLIDVSRNKALHGGNFQGTPIGVSM
DNTRLAIAAIGKLMFAQFSELVNDFYNNGLPSNL SGGRNP SLDYGFKGGEIAMASYCSE
LQFLANPVTNHVQSAEQHNQDVNSLGLISARKTAEAVDILKLMSS TYLVALCQSIDL RH
LEENMKSTVKNTVSQVAKKVLTMGVNGELHPSRFCEKD LLRVVDREYVFAYIDDVCSG
TYPLMQKLRQVLVDHALNNGETEKNTNTSIFQKIATFEEELKVLLPKEVEGVRIAYEND
TLSIPNRIKACRSYPLYRFVREELGRGFLTGEKVTSPGEEFDRVFTAMCKGQIIDPLLECL
GGWNGEPLPIC"

Figure 6

Sequence I.D. No. 1

Figure 7

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PAL2

MGSTEMEVD SHQNGERA EFCVKG DPLNWGMAAESLK GSHLDE
VKRMVAEFRKPVVRLGGETLT V SQVAAIAASDNAGVKVELSET
ARAGVKASSDWVMESMNKGTDSYGVTTGFGATSHRRTKEGGA
LQKELIRFLNAGIFGNGTESTHTLPHSATRAAMLVRINTLLQGY
SGIRFEILEAITKFLNHNVT PFLPLRG TITASGDLVPLSYIAGLLT
GRANSKAVGPTGEVLNAEKAF AEAGVEGGFFELQPKEGLALV
NGTAVGSGMASMVLF DANVLALLSEVL SAIFAEVMQ GKPEFTD
HLTHKLKHHPGQIEAAAIMEYILDGSDYV KAAQKVHEMDPLQ
KPKQDRYALRTSPQWLGPQIEVIRSSTKMIEREINSVNDNPLID
VSRNKALHGGNFQGTPIGV SMDNTRLAIAAIGKLMFAQFSELV
NDFYNNGLPSNLSGGRNPSLDYGFKGAEIAMASYCSELQFLAN
PVTNHVQSAEQHNQDVNSLGLISARKTAESVEILKLMSTTYLV
ALCQSIDLRHLEENLKSTVKNTVSLVAKKILTTGVNGELHPSRF
CEKDLLRVVDREYVFAYIDDACSATYPLMQKLRQVIVDHALN
NENDAGTSIFQKISEFEEELKAVLPKEVEGVRSAYESSTLTIPNR
IKECRSYPLYRFVREELGTGFLTGE EVTSPGEEFDKVFTALCKG
HIIDPLLEC VQGWNGVPLPIS

Figure 8

Sequence I.D. No. 2

1	MENGT	HVNG	SL	NG	FC	IK	DP	LN	WG	VA	AE	ALT	GS	HL	DE	VK	KK	MM	VE	FR	K	P	V	K
1	MENGN	HVNG	VW	ME	FC	IK	DP	LN	WG	VA	AE	ALT	GS	HL	DE	VK	KK	MM	VE	FR	K	P	V	K
51	LG	ET	LT	VS	QV	AG	IS	AG	DC	NM	WV	EL	SE	AA	RA	GV	KA	SS	DW	ME	SM	NK	GT	
51	LG	ET	LT	VS	QV	AG	IS	AG	DC	NM	WV	EL	SE	AA	RA	GV	KA	SS	DW	ME	SM	NK	GT	
101	DS	YGV	TT	GF	AT	SH	RR	TK	NG	GA	LO	KE	LI	RF	LN	AG	IF	GN	GT	ES	SH	TL	PH	SA
101	DS	YGV	TT	GF	AT	SH	RR	TK	NG	GA	LO	KE	LI	RF	LN	AG	IF	GN	GT	ES	SH	TL	PH	SA
151	TR	AA	ML	VR	IN	TL	LO	GY	SG	IR	FE	IL	EA	IT	KL	NN	IT	PL	RG	TI	AS	GD		
151	TR	AA	ML	VR	IN	TL	LO	GY	SG	IR	FE	IL	EA	IT	KL	NN	IT	PL	RG	TI	AS	GD		
201	LV	PL	SY	IA	GL	LT	GR	PN	SK	AV	GP	AGE	V	LN	AE	SA	FA	OA	GE	VE	GG	FE	LO	PK
201	LV	PL	SY	IA	GL	LT	GR	PN	SK	AV	GP	AGE	V	LN	AE	SA	FA	OA	GE	VE	GG	FE	LO	PK
251	LA	LV	NG	TA	VG	SG	MA	SM	VL	FE	AN	VL	AL	SE	V	LS	AI	FA	EV	MO	GK	PE	FT	DH
251	LA	LV	NG	TA	VG	SG	MA	SM	VL	FE	AN	VL	AL	SE	V	LS	AI	FA	EV	MO	GK	PE	FT	DH
301	HK	LK	HH	PG	IE	AA	AI	ME	YI	LD	GS	DY	KA	AK	OK	VH	EM	DP	LO	KP	KO	DR	YA	LR
301	HK	LK	HH	PG	IE	AA	AI	ME	YI	LD	GS	DY	KA	AK	OK	VH	EM	DP	LO	KP	KO	DR	YA	LR
351	SP	OW	LG	PO	IE	VI	RS	AT	KM	IE	RE	IN	S	V	N	D	N	P	LI	DV	S	R	NK	AL
351	SP	OW	LG	PO	IE	VI	RS	AT	KM	IE	RE	IN	S	V	N	D	N	P	LI	DV	S	R	NK	AL
401	GV	SM	DN	TR	LA	IA	AI	GK	VT	IA	OE	SE	L	V	N	D	EY	NN	GI	PS	HL	SG	GR	NP
401	GV	SM	DN	TR	LA	IA	AI	GK	VT	IA	OE	SE	L	V	N	D	EY	NN	GI	PS	HL	SG	GR	NP
451	KG	GE	I	A	M	A	S	Y	C	S	E	L	O	F	L	A	N	P	V	T	N	H	V	O
451	KG	GE	I	A	M	A	S	Y	C	S	E	L	O	F	L	A	N	P	V	T	N	H	V	O
501	DIL	K	M	S	S	T	Y	L	V	A	L	C	O	S	I	D	L	R	H	L	E	E	N	M
501	DIL	K	M	S	S	T	Y	L	V	A	L	C	O	S	I	D	L	R	H	L	E	E	N	M
551	LH	PS	R	F	C	E	K	D	L	R	V	D	R	EY	V	E	A	Y	AD	PC	IT	TY	P	M
551	LH	PS	R	F	C	E	K	D	L	R	V	D	R	EY	V	E	A	Y	AD	PC	IT	TY	P	M
601	ET	E	K	N	A	N	T	S	I	F	O	K	I	A	T	E	D	E	L	K	A	L	P	K
601	ET	E	K	N	A	N	T	S	I	F	O	K	I	A	T	E	D	E	L	K	A	L	P	K
651	RS	Y	P	L	Y	R	F	V	R	E	L	G	G	A	-----									
651	RS	Y	P	L	Y	R	F	V	R	E	L	G	G	A	-----									
667	CG	W	N	G	E	P	L	P	T	C	-----													
701	CG	W	N	G	E	P	L	P	T	C	-----													

Figure 9

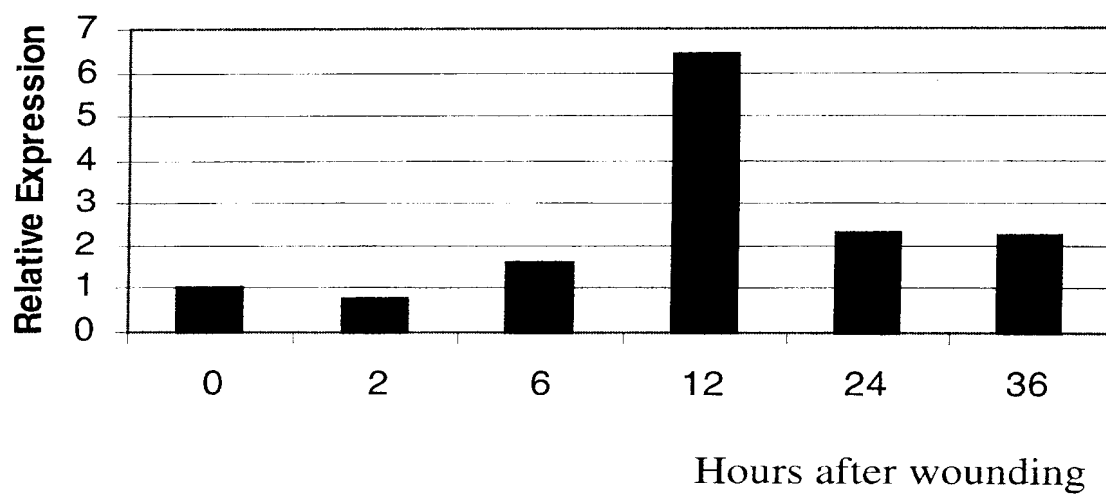
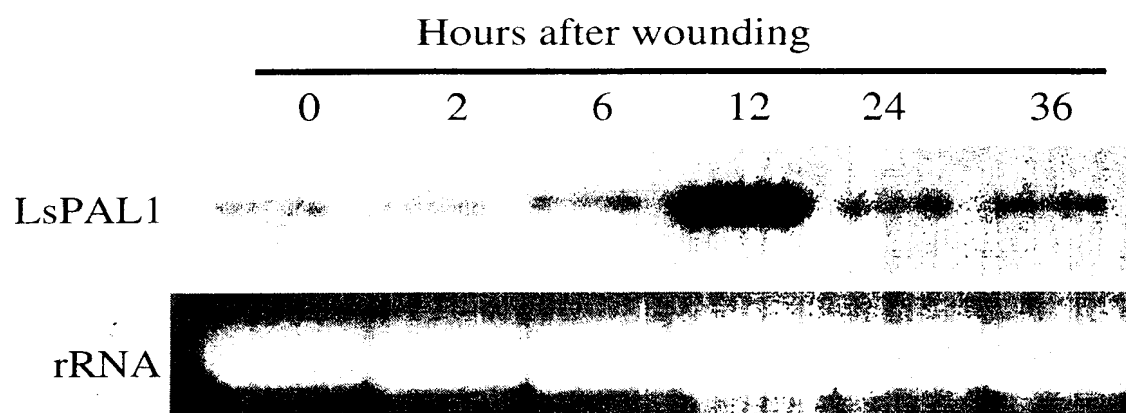


Figure 10

4

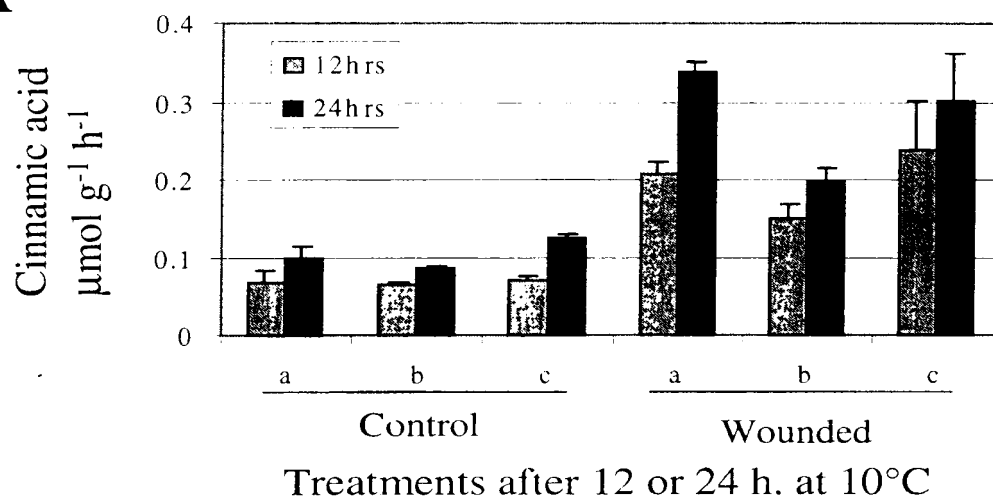
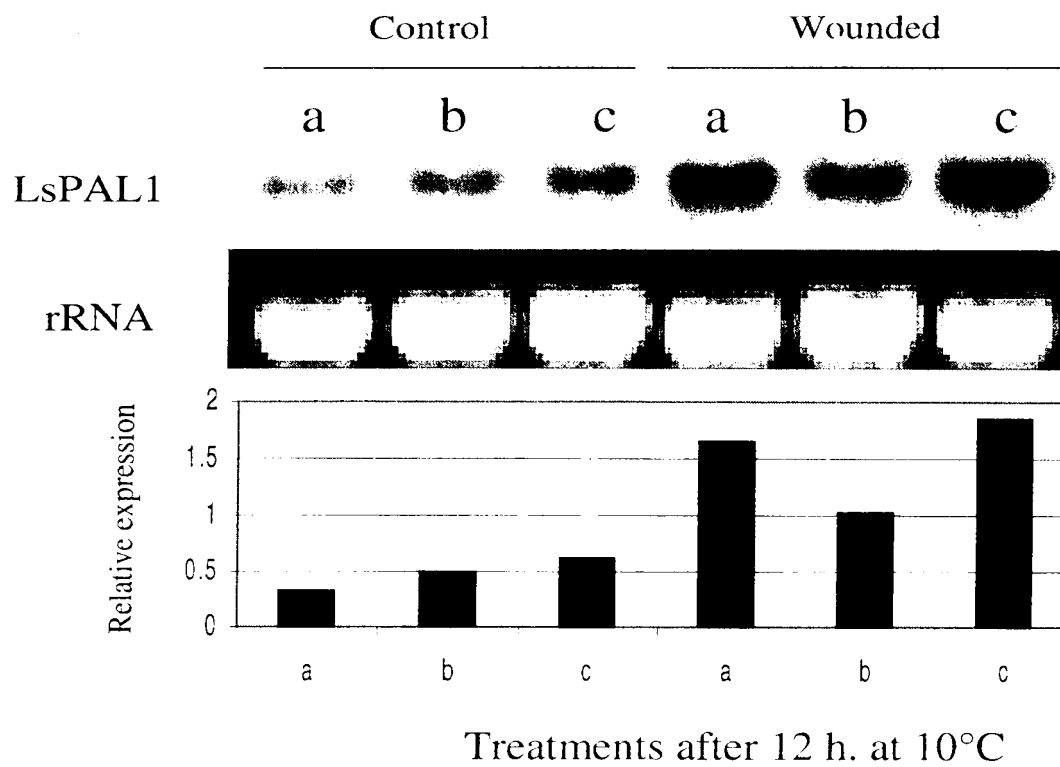
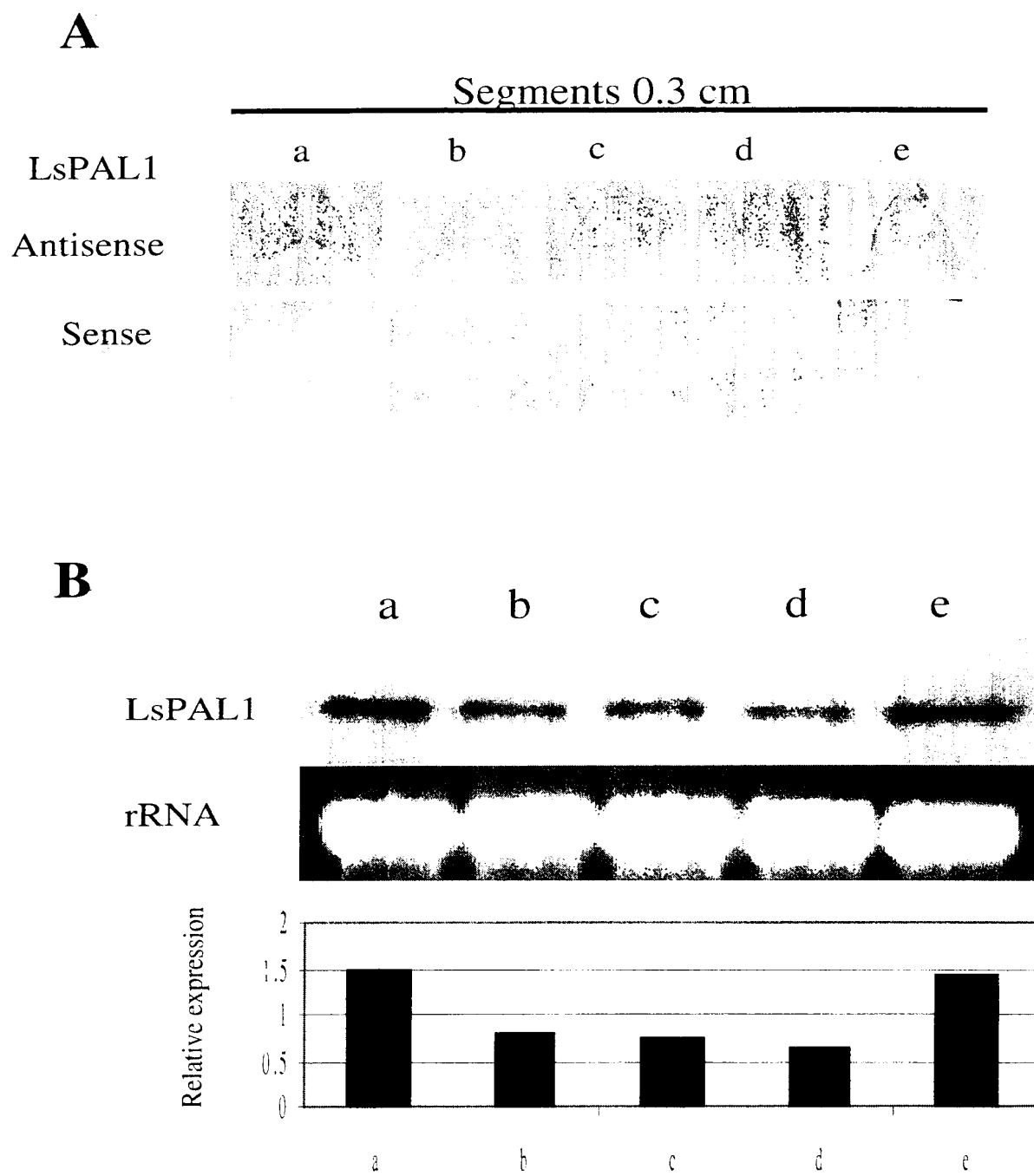
A**B**

Figure 11



Northern from pieces in A

Figure 12